

jc858 U.S. PTO
10/007267
12/03/01

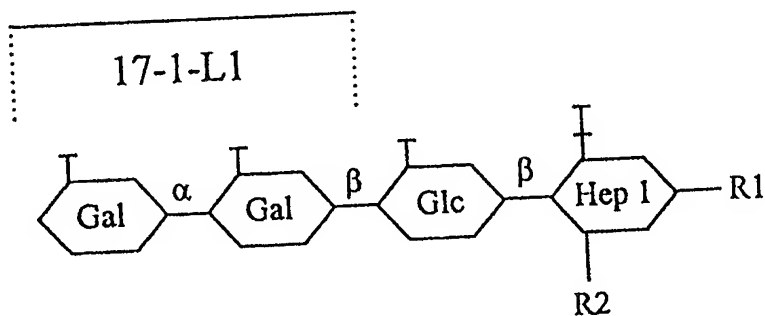
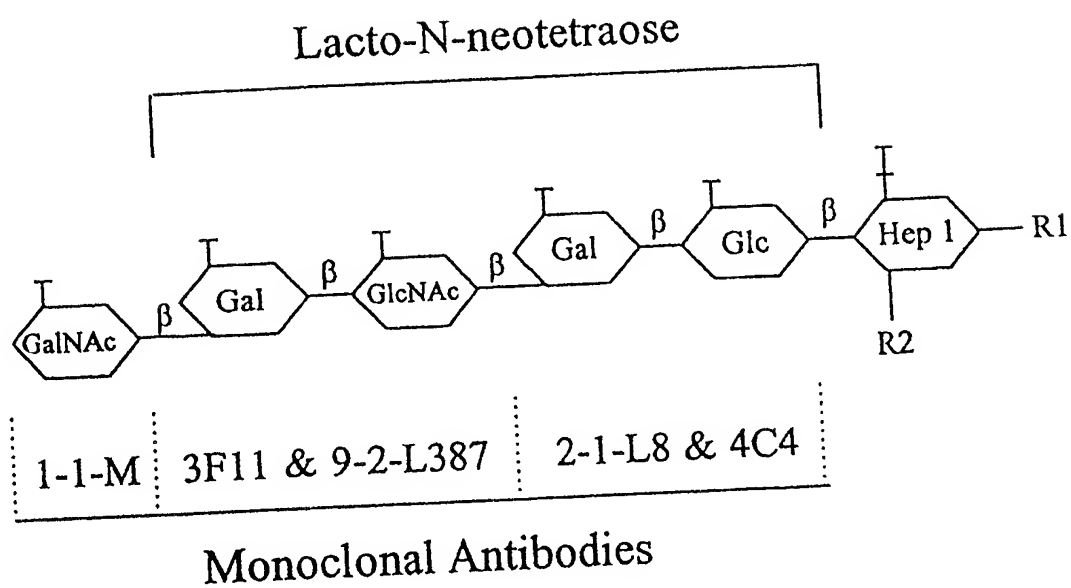


FIG. 1

LOS Locus

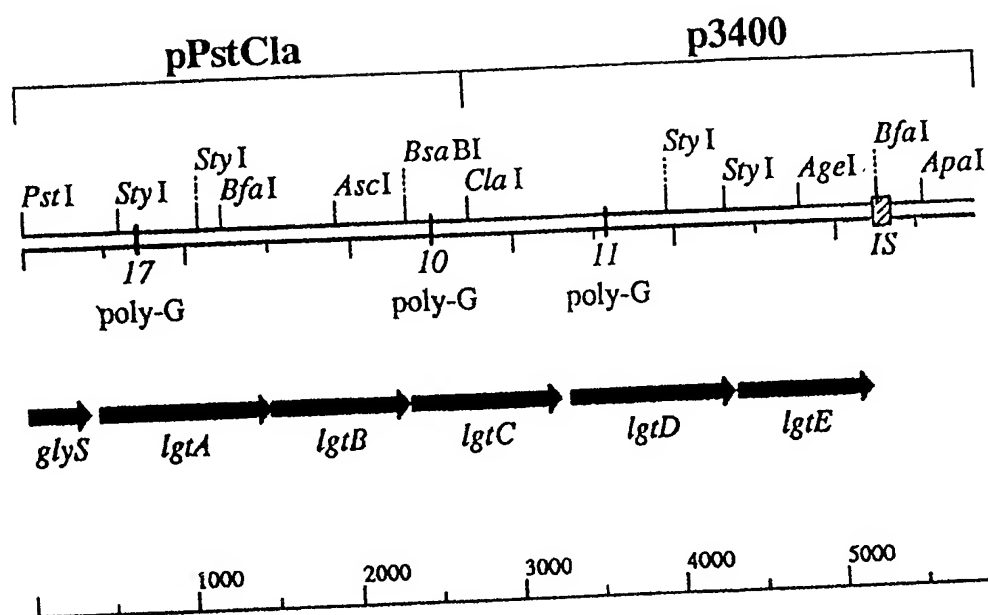


FIG.2A

FIG. 2B-1

SOURCE Neisseria gonorrhoeae.
 ORGANISM Neisseria gonorrhoeae
 source 1..5859

CDS
 <1..381
 /gene="glys"
 /codon_start=1
 /transl_table=11
 /product="glycyl tRNA synthetase beta chain"

/translation="LQAVAVFKQLPEAAALAAANKRVQNLLKKADAALGEVNESLLQQ
 DEEKALYAAAQGLQPKIAAAVAEGNFTALSELASVKPQVDAFFDGMVMAEDAAVKQ
 NRLNLLNRLAEQMNAVADIALLGE"

CDS
 445..1491
 /gene="lgtA"
 /codon_start=1
 /function="adds GlcNAc to lacto-N-neotetraose chain of
 gonococcal LOS"
 /evidence=experimental
 /transl_except=(pos:445..447,aa:Met)
 /transl_table=11
 /product="glycosyl transferase"

/translation="MQPLVSVLICAYNVEKYFAQSLAAVVNQVWRNLDILIVDDGSTD
 GTLAIKDFQKRDSRIKILAQANSGLIPLNIGLDELA KSGGGEYIARTDADDIA
 SPGWIEKIVGEMEKDRSIIAMGAWLEVLSEKDGNRRLARHKKHGIWKPTRHEDIAA
 FFPFGNPIHNNTMIMRRSVIDGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKY
 RLHANQVSSKHSVRQHEIAQGIQKTARNDFLQSMGFKTRFDSLEYRQTKAAAYELPEK
 DLPEEDFERARRFLYQCFKRTDTPPSGAWLDFAAADGRMRRLFTLRQYFGILYRLIKNR
 RQARSDSAGKEQEI"

FIG.2B-2

CDS

1491..2330
 /gene="lgtB"
 /codon_start=1
 /function="adds second galactose to the lacto-N-tetraose
 chain in LOS"
 /evidence=experimental
 /product="glycosyl transferase"

/translation="MQNHVISLASAAERRAHIAATFGSRGIPFQFFDALMPSERLERA
 MAELVPGLSAHPYLSGVEKACFMASHAVLWEQALDEGVPIAVFEDDVLLEGAEQFLA
 EDTWLQERFDPDSAFVVRLETMTMHVLTSPSGVADYGGRAFFLLESEHCCTAGYIISR
 KAMRFFLDRFAVLPPERLHPVDLMMFGNPDDREGMPVCQLNPALCAQELHYAKFHDQN
 SALGSLIEHRRRLNRKQQWRDSPANTFKHRLIRALTKIGREREKRRQRREQLIGKIIV
 PFQ"

CDS

2342..3262
 /gene="lgtC"
 /codon_start=1
 /function="adds galactose alpha(1-4) to Gal-Glc in
 gonococcal LOS"
 /evidence=experimental
 /transl_table=11
 /product="glycosyl transferase"

/translation="MDIVFAADDNYAAYLCAAKSVEAAHPDTEIRFHVLDAGISEEN
 RAAVAANLRGGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCCKVLYLD
 TDVLVRDGLKPLWDTDLGGNWVGACIDLFEVERQEGYKQKIGMADGEYFYNAGVLLINL
 KKWRRHDI FKMSCEWVEQYKDVMMQYQDDIILNGLFKGGVCYANSRNFMPNTNYAFMAN
 GFASRHTDPLYLDRNTAMPVAVSHYCGSAKFPWHRDCTVWGAERFTELAGSLTTVPPEE
 WRGKLAVPPTKCMQLQRWRKKLSARFLRKIY"

FIG.2B-3

```

CDS
3322..4335
/gene="lgtD"
/codon_start=1
/function="adds terminal GalNAc to lacto-N-neotetraose
chain of LOS"
/evidence=experimental
/transl_except=(pos:3322..3324,aa:Met)
/transl_table=11
/product="glycosyl transferase"

/translation="MQPLVSVLICAYNAEKYFAQSLAAVVGQWTRNLDILIVDDGSTD
GTPAIARHFQEQDGRIRIISNPRNLGFIASLNIGLDELAKSGGEYIARTDADDIASP
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PFGNPIHNNMTIMRRSVIDGGLRFPDPAITHAEDYKFWYEAGKLGRLAYYPEALVKYRF
HQDQTSKYNLQQRRTAWKIKEEIRAGYWKAAAGIAGADCLNYGLLKSTAYALYEKAL
SGQDIGCLRFLYEYFLSLEKYSLTDLDFLTDRVMRKLFAPQYRKILKKMLRPWKY
RSY"
CDS
4354..5196
/gene="lgtE"
/codon_start=1
/function="adds first galactose to lacto-N-neotetraose
chain of LOS"
/evidence=experimental
/transl_table=11
/product="glycosyl transferase"

/translation="MQNHVISLASAAERRAHIADTFGSRGIPFQFFDALMPSEERLEQA
MAELVPGLSAHPYLSGVEKACFMASHAVLWEQALDEGLPYIAVFEDDVLLGEGAEQFLA
EDTWLEERFDKDSAFIVRLETMTFAKVIVRPDKVLNYENRSFPLLESEHCGTAGYIISR
EAMRFFLDRAFVLPPEIRIKAVDLMFTYFFDKEGMPVYQVSPALCTQELHYAKFLSQN
SMLGSDLEKDREQGRRRHRRSLKVMFDLKRALGKFGREKKRMRERQRAELEKVGRRV
ILFK"

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FIG.2B-4

BASE COUNT	1412 a	1462 c	1661 g	1324 t	
ORIGIN					
1	ctgcaggccg	tcgccgtatt	caaacaactg	ccgaagccg	ccgcgctcgc
61	aaacgcgtgc	aaaacctgct	gaaaaaagcc	gatgcgcgt	tgggcgaagt
121	ctgctgcaac	aggacgaaga	aaagccctg	tacgctgccg	cgcaagggtt
181	attgcccgcg	ccgtcgccga	aggcaatttc	cgaaccgct	tgccggaact
241	aagccgcagg	ttgatgcctt	cttcgacggc	gtgatggtga	tgccggaaga
301	aaacaaaacc	gcctgaacct	gctgaaccgc	ttggcagagc	agatgaacgc
361	atcgcgcctt	tgggcgagta	accgttgtac	agtcctgaag	ccgtctgaag
421	gcatcaaat	atcgggagag	taaatcgag	cctttagtca	gcgtattgat
481	aacgtagaaa	aatatcttgc	ccaatcatta	gccgcgcgtc	tgaatcagac
541	ttggatat	tgattgtcga	tgacggctcg	acagacggca	cacttgccat
601	tttcaaaagc	gggacagccg	tataaaaac	ccttgacaa	ctcaaaatc
661	ccctctttaa	acatcgggct	ggacgaattg	gcaaagtcgg	gggggggggg
721	attgcgcgca	ccgatgccga	cgatatcgcc	tccccggct	ggattgagaa
781	gagatggaaa	aagaccgcag	catcattgcg	atgggcgcgt	ggctggaa
841	gaaaaggacg	gcaaccggct	ggcgcggcac	cacaaacacg	gcaaaattg
901	accgggcacg	aagacatcgc	cgctttttc	cctttcggca	acccatata
961	atgattatgc	ggcgacgcgt	cattgacggc	ggtttgcgtt	acgacaccca
1021	gcggaagatt	accaattttg	gtacgatgtc	agcaaatggg	gcaggctggc
1081	gaagccttgg	tcaaataccg	ccttcacgcc	aatcagggtt	catccaaaca
1141	caacacgaaa	tcgcgcaagg	catccaaaaa	accgcccaga	acgattttt
1201	ggttttaaaa	cccgggttcga	cagcctagaa	taccgcccga	caaaagcagc
1261	ctgcccggaga	aggattttgc	ggaagaagat	tttgaacgcg	ccgcgcggtt
1321	tgcttcaaac	ggacggacac	gccgccctcc	ggcgcgtggc	tggtttcgc
1381	aggatgaggg	ggctgtttac	cctgaggcaa	tacttcggca	ttttgtaccg
1441	aaccgcccgc	aggcgcggtc	ggattcggca	gggaaagaac	aggagattta
1501	acgttatcag	cttggcttcc	gccgcagaa	gcaggggcgca	cattgcgcga
1561	gtcgcggcat	cccgttccag	tttttcgacg	cactgatgcc	gtctgaaagg

FIG.2B-5

1621	caatggcgga	actcgtcccc	ggcttgctcg	cgcaccccta	tttgagcgga	gtggaaaaag
1681	cctgctttat	gagccacgcc	gtattgtggg	aacaggcatt	ggacgaaggc	gtaccgtata
1741	tcgcccgtatt	tgaagatgat	gtcttactcg	gcgaaggcgc	ggagcagttc	cttgccgaag
1801	atacttggct	gcaagaacgc	tttgaccccc	attccgcctt	tgtcgtccgc	ttggaacga
1861	tgtttatgca	ctcctgacc	tcgcccctcg	gcgtggcgga	ctacggcggg	cgcgccttcc
1921	cgctttttgga	aagcgaacac	tcggggacgg	cgggctatat	tatttccga	aaggcgatgc
1981	gtttttttctt	ggacagggtt	gccgttttgc	cgcccgaacg	cctgcacct	gtcgatttga
2041	tgatgttcgg	caaccctgac	gacagggaag	gaatgccggt	ttgccagctc	aatcccgcct
2101	tgtcgcccca	agagctgcat	tatgccaaagt	ttcacgacca	aaacagcgca	ttgggcagcc
2161	tgatcgaaca	tgaccgccgc	ctgaaccgca	aacagcaatg	gcgcgattcc	ccgcaccaac
2221	cattcaaaaca	ccgcctgac	cgcccttga	ccaaaatcgg	cagggaagg	gaaaaacgcc
2281	ggcaaaagcg	cgaacagtta	atcggcaaga	ttattgtgcc	tttccaataa	aaggagaaaa
2341	gatggacatc	gtatttgcgg	cagacgacaa	ctatgccgcc	tacctttgcg	ttgcggcaaa
2401	aagcgtggaa	gcggcccatc	ccgatacggg	aatcaggttc	cacgtcctcg	atgccggcat
2461	cagtaggaa	aaccgggcgg	cggttgccgc	caatttgcgg	ggggggggta	atatccgctt
2521	tatagacgta	aaccgcgaag	attcgcgcgg	ctccccctta	aacatcaggc	acatttccat
2581	tacgacttat	gcccgcctga	aattgggcga	atacatggcc	gattgcgaca	aagtcctgta
2641	tctggatacg	gacgtattgg	tcagggacgg	cctgaagccc	ttatgggata	ccgatttggg
2701	cggtaaactgg	gtcggcgcg	gcatcgattt	gtttgtcgaa	aggcagggaag	gatacaaca
2761	aaaaatcgg	atggcggacg	gagaatat	tttcaatgcc	ggcgtattgc	tgatcaacct
2821	gaaaaagtgg	cggcggcacg	atattttcaa	aatgtcctgc	gaatgggtgg	acaatacaaa
2881	ggacgtgatg	caatatcagg	atcaggacat	tttgaacggg	ctgttttaag	gcggggtgtg
2941	ttatgcgaac	agccgtttca	actttatgcc	gaccaattat	gccttttatgg	cgaacgggtt
3001	tcgctcccc	cataccgacc	cgctttacct	cgaccgtacc	aatacggcga	tgcccgtcgc
3061	cgtcagccat	tattgcggct	cgccaaagcc	gtggcacagg	gactgcaccg	tttgggggtgc
3121	ggaacgtttc	acagagtggg	ccggcagcct	gacgaccgtt	ccgaaagaat	ggcgcgggcaa
3181	acttgcgctc	ccgccgacaa	agtgtatgct	tcaaatgg	cgcaaaaagc	tgtctgccag
3241	attcttacgc	aagatttatt	gacggggcag	gccgtctgaa	gccttcagac	ggcatcggac
3301	gtatcggaac	ggagaaacgg	attgcagcct	ttagtcagcg	tattgatttg	cgcctacaac
3361	gcagaaaaat	atattgcccc	atcattggcc	gccgtagtgg	ggcagacttg	gcgcaacttg

FIG.2B-6

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3421 gataatttga ttgtcgatga cggctcgacg gacggcacgc cggccattgc cgggcatttc
3481 caagaacagg acggcaggat caggataatt tccaatcccc gcaatttggg ctttatcgcc
3541 tctttaaaca tcgggctgga cgaattggca aagtcggggg ggggggaata tattgcgcgc
3601 accgatgccg acgatatatgc acgatatatgc ctcccccgcc tggattgaga aaatcgtggg cgagatggaa
3661 aaagaccgca gcatcatatgc gcatcatatgc gatggcgccg tggttggaag ttttgcgga agaaaaaat
3721 aaaagcgtgc ttgcccgcac ttgcccgcac tgcccgaattt ggcgcaattt gggacaacac gaccggcat
3781 gaagacattg tcgcccgttt tcgcccgttt ccccttcggc aaccccatc acaacaacac gatgattatg
3841 aggcgcagcg tcattgacgg tcattgacgg cggtttgcgg ttcgatccag cctatatcca gccgaagac
3901 tataagtatt ggtacgaagc ggtacgaagc cggcaaaactg ggcaggctgg ctattatcc cgaagccttg
3961 gtcaaatacc gcttccatca agaccagact tcttccaaat tcttccaaat acaacctgca acagcgagg
4021 acggcgtgga aaatcaaga agaaatcagg gcgggggtatt ggaaggcgcc ggcataatgc aggcatagcc
4081 gtggggcgcg actgcctgaa ttacgggctt ttgaaatcaa ttgaaatcaa cgcataatgc ggtgtacgaa
4141 aaagccttgt ccggacagga tatcggatgc ctccgcctgt ctccgcctgt tgacagaccg cgtgatgagg
4201 tcgttggaaa agtatcttct ccgcaccgca atataggaaa atcctgaaaa atcctgttac cagcttggct
4261 aagctgtttg accgcagct attgaaaccg gcacattgcc gacatttgc gagtcgccc catccgttc
4321 taccgcagct tccgcgcag acgcactgat acgcactgat ggcgtctgaa aggcgggaa atacgcttat
4381 tccgcgcag cagtttttcg cggcgaccc cgttggatgaa ggtctgccc ggagtggaaa atatcgcctt
4441 cagtttttcg cggcgaccc cgttggatgaa ggtctgccc ggagtggaaa atatcgcctt
4501 cggcgaccc cgttggatgaa ggtctgccc ggagtggaaa atatcgcctt
4561 ggcgtattgt ggcgtattgt ggcgtattgt ggcgtattgt ggcgtattgt ggcgtattgt
4621 gacgttttac gacgttttac gacgttttac gacgttttac gacgttttac gacgttttac
4681 cgttttgaca cgttttgaca cgttttgaca cgttttgaca cgttttgaca cgttttgaca
4741 gtcagaccgg gtcagaccgg gtcagaccgg gtcagaccgg gtcagaccgg gtcagaccgg
4801 cattgtggga cattgtggga cattgtggga cattgtggga cattgtggga cattgtggga
4861 ttgcccgttt ttgcccgttt ttgcccgttt ttgcccgttt ttgcccgttt ttgcccgttt
4921 ttgataaagg ttgataaagg ttgataaagg ttgataaagg ttgataaagg ttgataaagg
4981 cattatgcca cattatgcca cattatgcca cattatgcca cattatgcca cattatgcca
5041 gaacaaggaa gaacaaggaa gaacaaggaa gaacaaggaa gaacaaggaa gaacaaggaa
5101 ggtaaattcg ggtaaattcg ggtaaattcg ggtaaattcg ggtaaattcg ggtaaattcg
5161 aaagtttacg aaagtttacg aaagtttacg aaagtttacg aaagtttacg aaagtttacg

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FIG.2B-7

5221 aatcagaaat ggacacactg tcattcccgc gcaggcggga atctagggtct ttaacttcg
5281 gttttttccg ataaattctt gccgcattaa aattccagat tcccgccttc gcggggatga
5341 cggcggggg atgttgctt ttccggataa aatcccgtgt tttttcatct gctaggtaaa
5401 atcgcccaa agcgtctgca tcgcggcgat gccggcttca aatgacctgtt gttcttcctg
5461 aatccgtttt ccgagtgtaa ccgcctcgg gccgacctt aaagacgatt gcgccggacg ggtggcggat
5521 ttctgtccag ccgccttcgg ggttgatgct cataatcagc ttggtgtttt cagacggcat
5581 gtccgcgagt ttgcaggcgc agccgatgat gggcagtagc gggggaacgg tgttcctgcc
5641 ttgttcgagt gcttcacggt cagcggaga tgacgatttc ctgccagcgt gcgaggcgtt tggcggcgcg
5701 gctttgttcg cagcggaga tgcagcgttc gctgatgacg ggctgtatgg cggttacgcc
5761 ttctccgtcg aggcggacga tgcagcgttc gctgatgacg ggctgtatgg cggttacgcc
5821 gagtccgacg cttttttgca ggtgaaatc catgcgac

1gtB 1 MQNHV ISLASAAERRAH IADTFGSRGIPFQFFDALMPSERLEQAMAE LVP 50
|||||
1gtE 1 MQNHV ISLASAAERRAH IADTFGSRGIPFQFFDALMPSERLEQAMAE LVP 50
|||||
1gtB 51 GLSAHL YLSGVEKACFM SHAVLWEQALDEGLPYIAVFEDD VLLGEGAEQF 100
|||||
1gtE 51 GLSAHP YLSGVEKACFM SHAVLWEQALDEGLPYIAVFEDD VLLGEGAEQF 100
|||||
1gtB 101 LAEDTWLQERFDPDSAFVVRLETMFMHVL TSPSGVADYGGRAFPLLESEH 150
|||||
1gtE 101 LAEDTWLEERFDKDSAFIVRLETMFAKVIVRPDKVLNYENRSFPLLESEH 150
|||||
1gtB 151 CGTAGY IISRKAMRFFLD RFAVLPPERLHPVDLMMFGNPDDREGMPVCQL 200
|||||
1gtE 151 CGTAGY IISREAMRFFLD RFAVLPPERIKAVDLMMF TYFFDKEGMPVYQV 200
|||||

FIG.4A

1gtB 201 NPALCAQELHYAKFHDQNSALGSLIEHRRRLNRKQQRDSPANTFKHRLI 250

1gtE 201 SPALCTQELHYAKFLSQNSMLGSDLEKD REQGRRHRRSLKVMFDLK 246

1gtB 251 RALTKIGREREKRRKRR EQTIGKIIIVPFQ 279

1gtE 247 RALGKFGREKKRMERQORQAELEKVYGRRVILFK 280

FIG.4B

rfaI 29 LDIAYGTDKNFLFGCGISIASILKYNEGSRLCFHIFTDYFGDDDRKYFDA 78
1 MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEENRAAVAA 50
rfaI 79 LALQYKTRIKIYLINGDRLRLSP.STKNWTHAIYFRFVIADYFINKAPKV 127
1gtc 51 .NLRGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEY.IADCCKV 98
rfaI 128 LYLDADIICQGTIEPLINFSFPDDKVAMVV...TEGQADWWEKRAHSLGV 174
1gtc 99 LYLDTDVLVRDGLKPLWDTDLGGNWWGACIDL FVERQEGYKQK....IGM 144
rfaI 175 AGIAKGYFNSGFLINTAQWAAQQVSARAIAMLNEPEIIKKITHPDQDVL 224
1gtc 145 AD.GEYFYNAGVLLINLKKWRRHDIFKMSCEWVEQKDV MQ..YQDQDIL 191

FIG.5A

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rfaI 225 NMLLADKLIFADIKYNTQFSLNYQLKESFINPVTNDTIFI..... 264
      ||| : : : : : : : : : : : : : : : : : : : : : : : : :
1gtC 192 NGLFKGGVCYANSRFNF.MPTNYAFMANGFASRHTDPLYLDRNTAMPVA 240
      ||| : : : : : : : : : : : : : : : : : : : : : : : : :

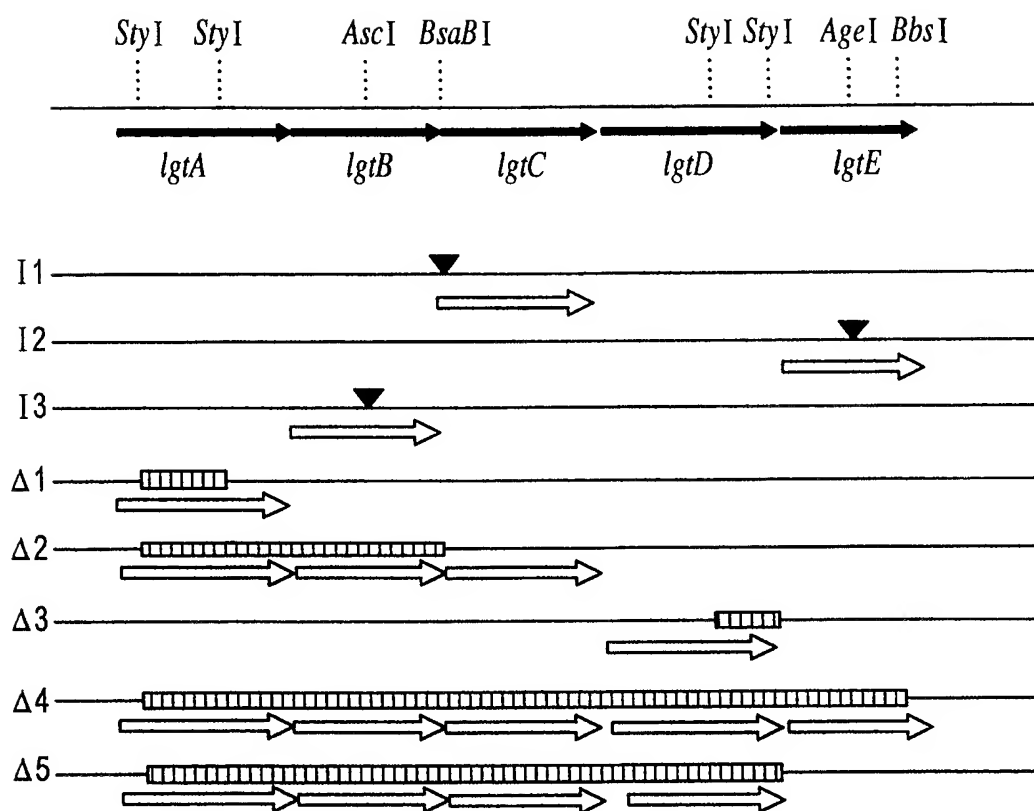
rfaI 265 ..HYIGPTKPWHDWAWDYPVSQAFMEAKNASPWKNNTALLKPNNSQLRYS 312
      ||| : : : : : : : : : : : : : : : : : : : : : : : : :
1gtC 241 VSHYCGSAKPWH...RDCTVWGAERFTELAGSL..TTVPEEWRGKLAVPP 285
      ||| : : : : : : : : : : : : : : : : : : : : : : : : :

rfaI 313 AKHMLKKHRYLKGFSNYLFYFI 334
      ||| : : : : : : : : : : : : : : : : : : : : : : : : :
1gtC 286 TKCML..QRWRKKLSARFLRKI 305
      ||| : : : : : : : : : : : : : : : : : : : : : : : : :

```

FIG. 5B

FIG.6



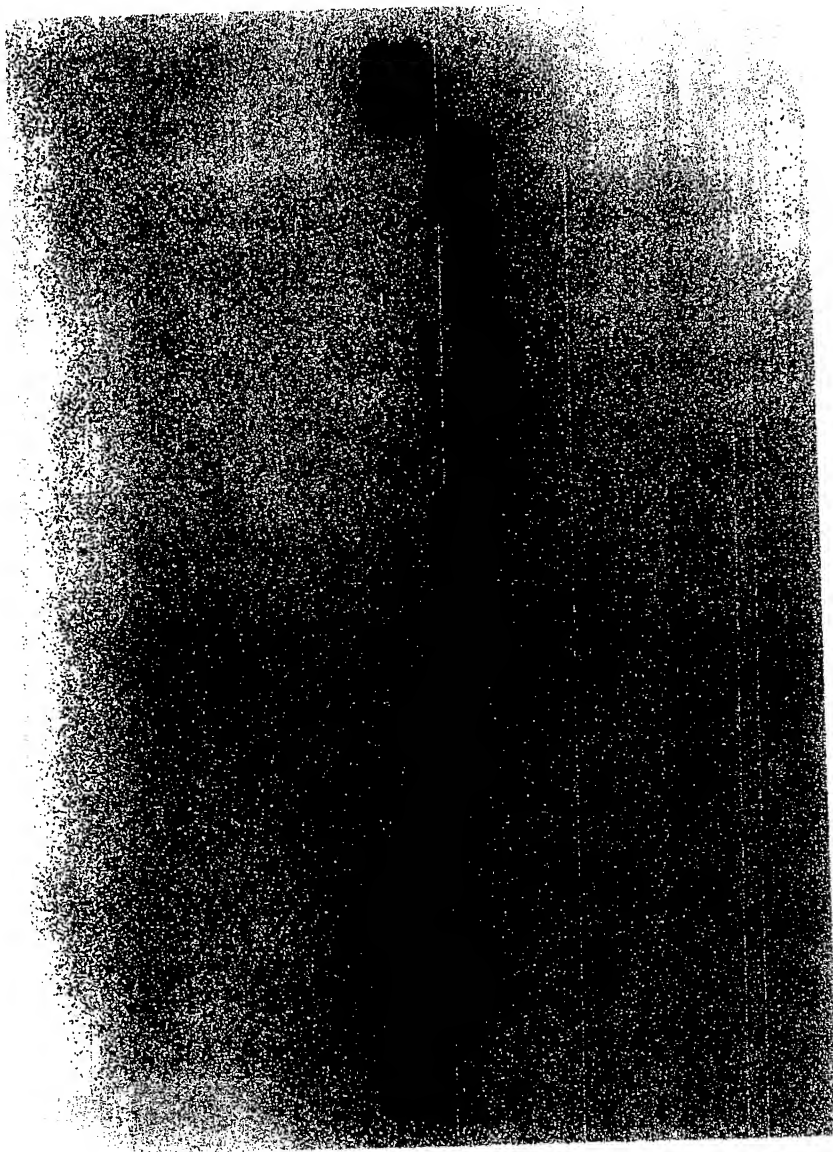


FIG. 7

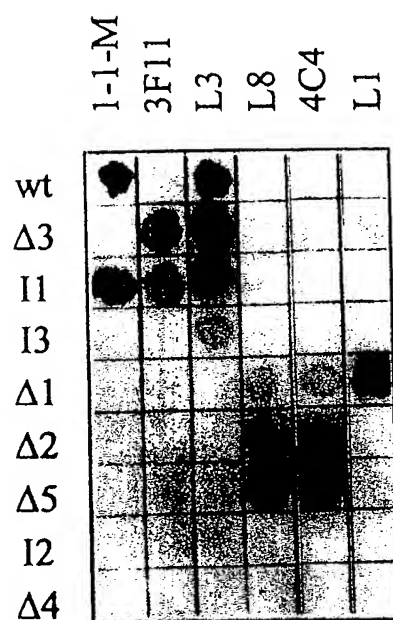


FIG.8